Dr. Hongmei Zhang, associate professor in the Division of Epidemiology, Biostatistics, and Environmental Health and coordinator of the Biostatistics Program at the University of Memphis School of Public Health, has been awarded an R01 grant by the National Institute of Allergy and Infectious Diseases (NIAID) of National Institutes of Health with a preliminary study funded by the Asthma and Allergy Foundation of America for the study of epigenetic methylation and the gender-switch in adolescent asthma.

Does Epigenetic Methylation Explain the Gender-Switch In Adolescent Asthma?

Early prevention of asthma is essential to reduce the burden of this high-impact and avoidable disease. Asthma is more common in boys among pre-teenagers, but during adolescence it becomes more common in girls. This “switch-over” is likely caused by factors that influence gene activities, e.g., DNA methylation of nucleotides. DNA methylation does not alter genes but is a process of putting some (strong or weaker) chemical marks on the nucleotides. The strength of the marks can be changed and consequently will make genes less or more expressed (and thus influence the risk of asthma). In our study, we will 1) assess genome-wide DNA methylation of specific nucleotides called CpG sites using blood samples taken before and after adolescent transition; for each gender we will identify specific DNA methylation that is associated with asthma status change during adolescent transition; 2) test the association of DNA methylation with asthma risk factors (growth changes, use of contraceptives and pain killers, and smoking). This assessment will identify asthma risk factors that influence DNA methylation; 3) evaluate the agreement of methylation in peripheral blood leukocytes (PBL) and bronchial epithelial cells (BEC), and in PBL and in BEC, functionally assess the identified epigenetic marks in cis and trans via gene expressions and risk factors.

The findings from the projects have strong potential to critically impact our ability to prevent incidence and promote remission of asthma during adolescence. In the meantime, we will develop efficient statistical analysis tools for analyzing longitudinal data in genome scale, which will bring potential to advance statistical methodology in the bioinformatics area.